

Alignment of SSC nectin1 extra cellular domain(VCC), as defined in sequence 2 and bovine nectin1 extracellular domain (as from gi:XP612918)

Multalin version 5.4.1

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Published research using this software should cite

Multiple sequence alignment with hierarchical clustering

F. CORPET, 1988, Nucl. Acids Res., 16 (22), 10881-10890

Symbol comparison table: blosum62

Gap weight: 12

Gap length weight: 2

Consensus levels: high=90% low=50%

Consensus symbols:

! is anyone of IV

\$ is anyone of LM

% is anyone of FY

is anyone of NDQEBZ

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MSF:      336      Check:      0      ..
Name: SSC-ECD(seq.2) Len:      336 Check: 8371 Weight: 1.00
Name: BTA-ECD(gi:XP612918) Len:      336 Check: 8260 Weight: 1.00
Name: Consensus      Len:      336 Check: 4256 Weight: 0.00

      1
SSC-ECD(seq.2) MARMGLAGAA GRWWGLALGL TAFFLPGAHT QVVQVNDSMY GFIGTDVVLH
BTA-ECD(gi:XP612918) MARMGLAGAA GRWWGLALGL TAFFLPGAQA QMVQVNDSMY GFIGTDVVLH
Consensus      MARMGLAGAA GRWWGLALGL TAFFLPGAga QmVQVNDSMY GFIGTDVVLH

      51
SSC-ECD(seq.2) CSFANPLPGV KITQVTWQKA TNGSKQNVAI YNPAMGVSVL APYRERVEFL
BTA-ECD(gi:XP612918) CSFANPLPGV KITQVTWQKA TNGSKQNVAI YNPAMGVSVL APYRERVEFL
Consensus      CSFANPLPGV KITQVTWQKA TNGSKQNVAI YNPAMGVSVL APYRERVEFL

      101
SSC-ECD(seq.2) RPSFTDGTIR LSRLELEDEG VYICEFATFP AGNRESQLNL TVMAKPTNWI
BTA-ECD(gi:XP612918) RPSFTDGTIR LSRLELEDEG VYICEFATFP AGNRESQLNL TVMAKPTNWI
Consensus      RPSFTDGTIR LSRLELEDEG VYICEFATFP AGNRESQLNL TVMAKPTNWI

      151
SSC-ECD(seq.2) EGTQAVLRAR KGKDDKVLVA TCTSANGKPP SVVSWETHLK GEAEYQEIRN
BTA-ECD(gi:XP612918) EGTHAVLRAR KGQDEKVLVA TCTSANGKPP SVVSWETRLK GEAEYQEIRN
Consensus      EGTqAVLRar KGqD#KVLVA TCTSANGKPP SVVSWETrLK GEAEYQEIRN

      201
SSC-ECD(seq.2) PNGTVTVISR YRLVPSREDH RQSLACIVNY HMDRFRESLT LNVQYEPEVT
BTA-ECD(gi:XP612918) PNGTVTVISR YRLVPSREAH RQSLACIVNY HMDRFWESLT LNVQYEPEVT
Consensus      PNGTVTVISR YRLVPSREah RQSLACIVNY HMDRFrESLT LNVQYEPEVT

      251
SSC-ECD(seq.2) IEGFDGNWYL QRMDVKLTCK ADANPPATEY HWTTLNGSLP KGVEAQNRTL
BTA-ECD(gi:XP612918) IEGFDGNWYL QRMDVKLTCK ADANPPATEY HWTTLNGSLP KGVEAQNRTL
Consensus      IEGFDGNWYL QRMDVKLTCK ADANPPATEY HWTTLNGSLP KGVEAQNRTL

      301
SSC-ECD(seq.2) FFRGPPINYSM AGTYICEATN PIGTRSGQVE VNITEF
BTA-ECD(gi:XP612918) FFRGPPINYSL AGTYVCEATN PIGTRSAQVE VNITEF
Consensus      FFRGPPINYS$ AGTY!CEATN PIGTRSaQVE VNITEF
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13 aa.changes over 336 residues